

FIGURE 1A

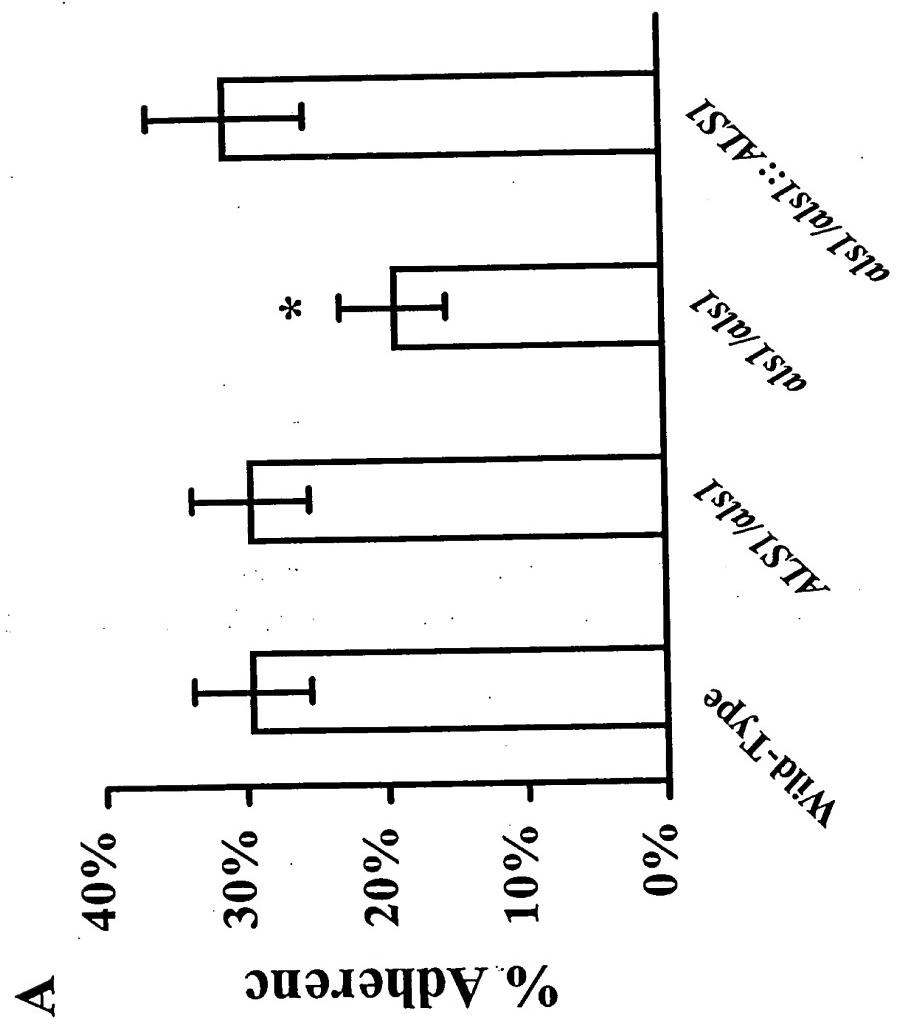
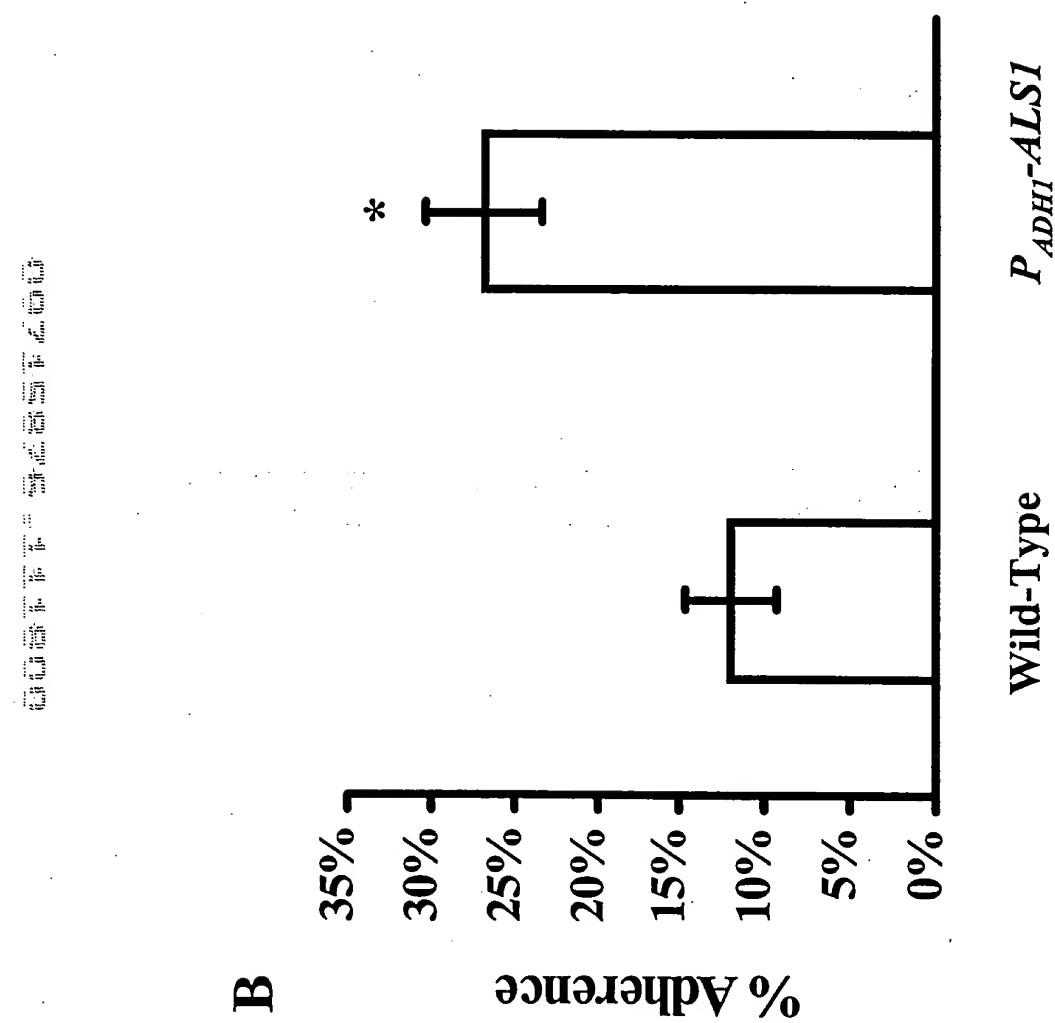
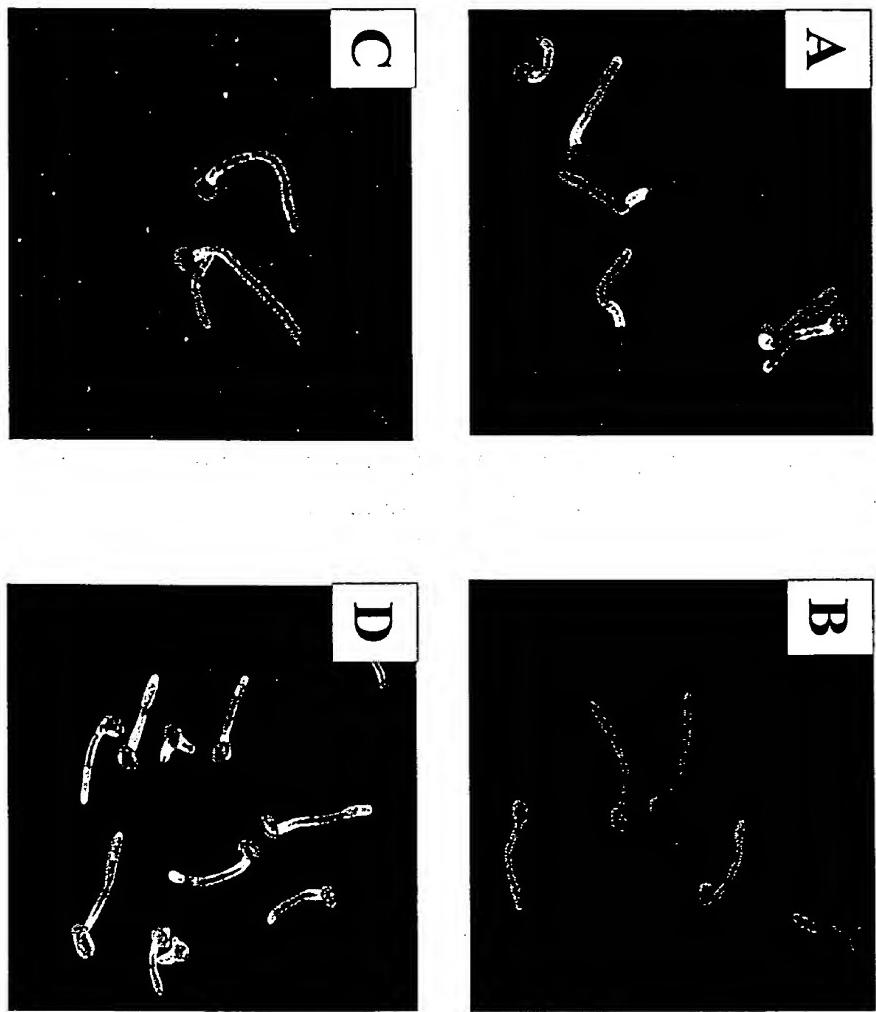


FIGURE 1B



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FIGURES 2A, 2B, 2C, 2D

FIGURE 3A

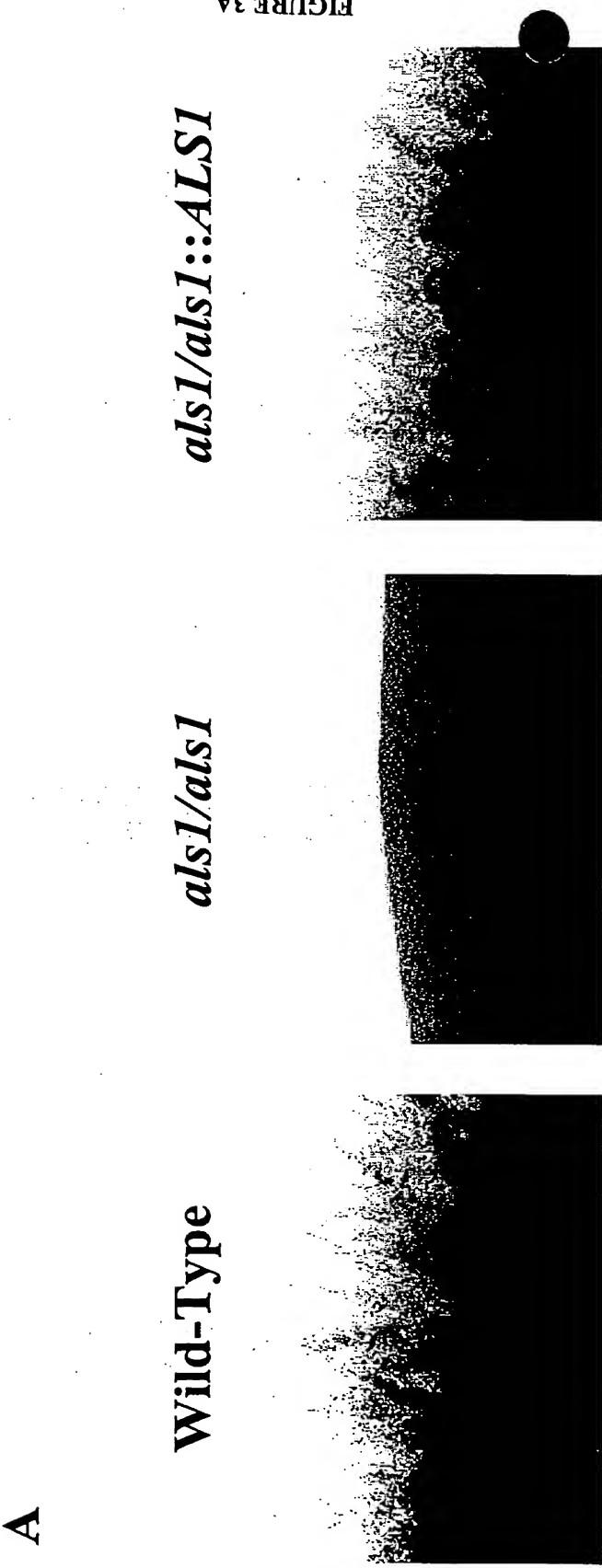
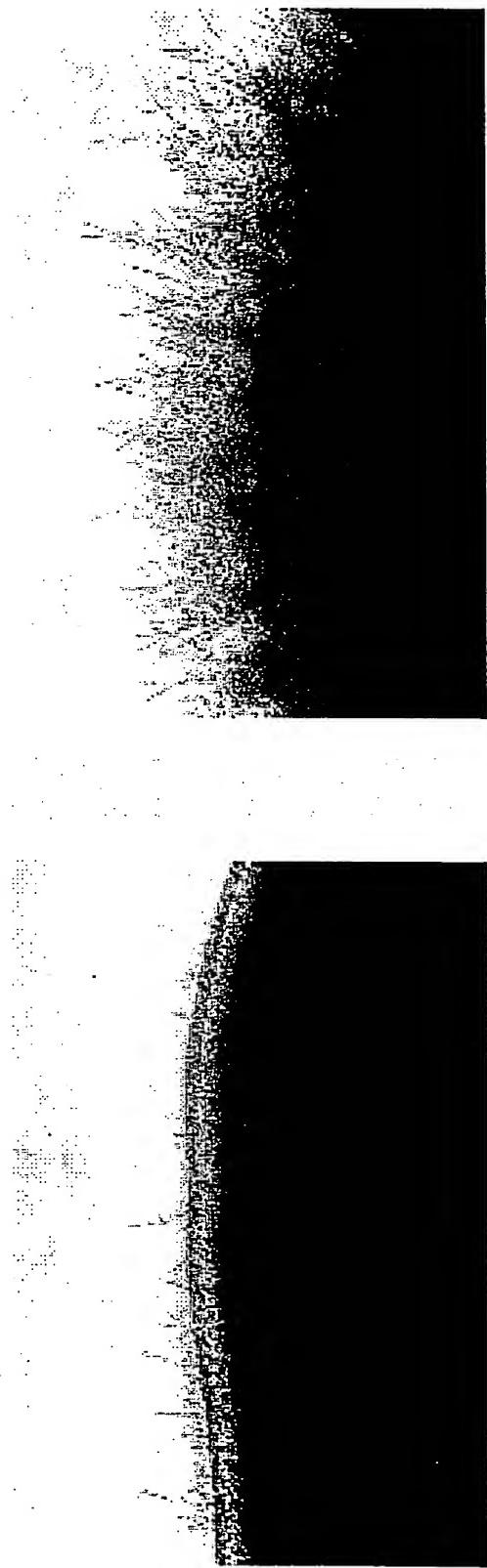


FIGURE 3B

$P_{ADHI-ALS1}$

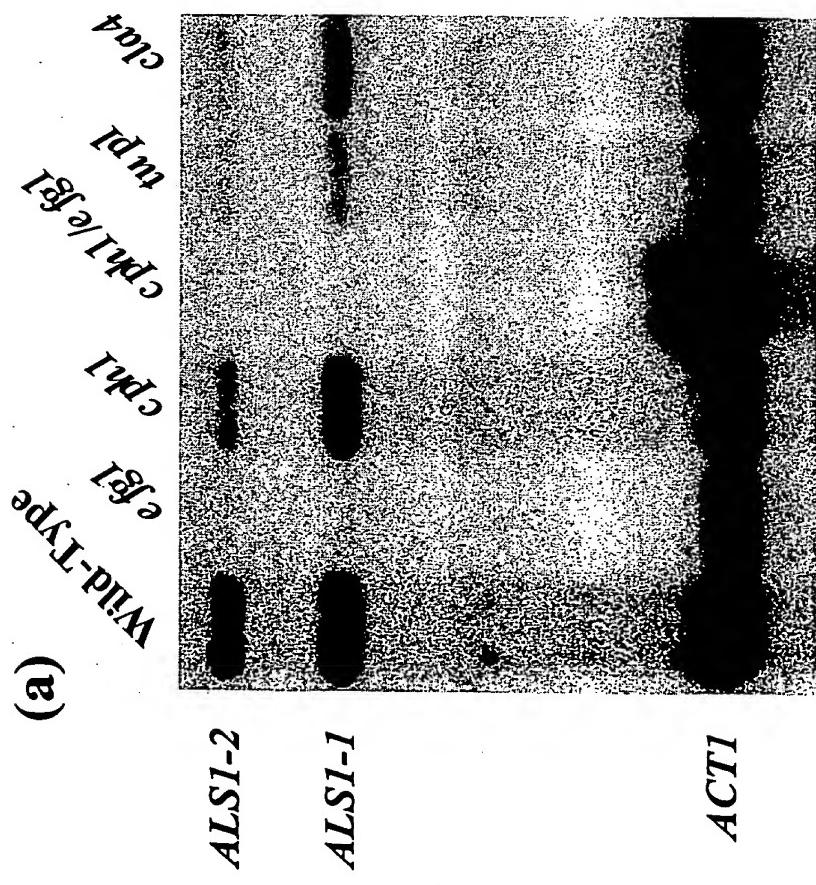
Wild-Type

B

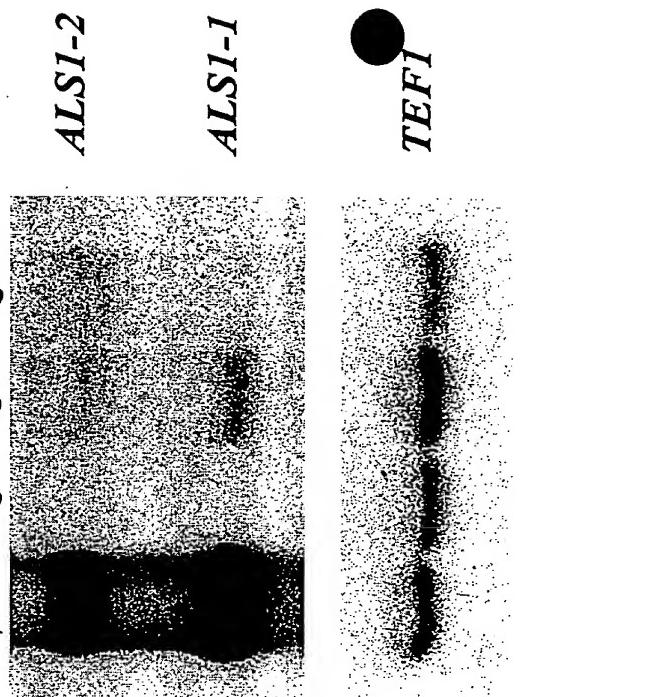


RESULTS AND DISCUSSION

A



(b)



RESULTS 4A

FIGURE 4B

*efg1/efg1, P<sub>ADH1</sub> ALS1*

B

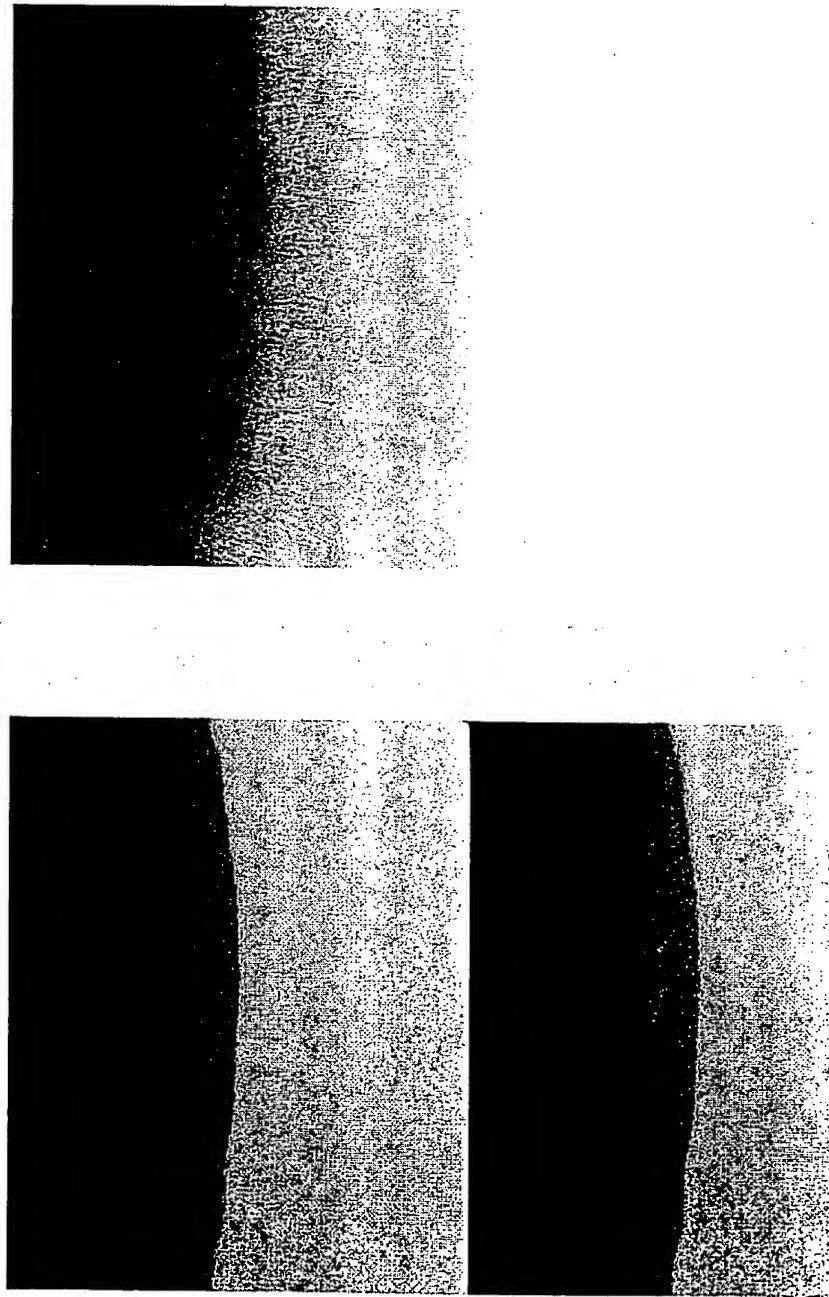
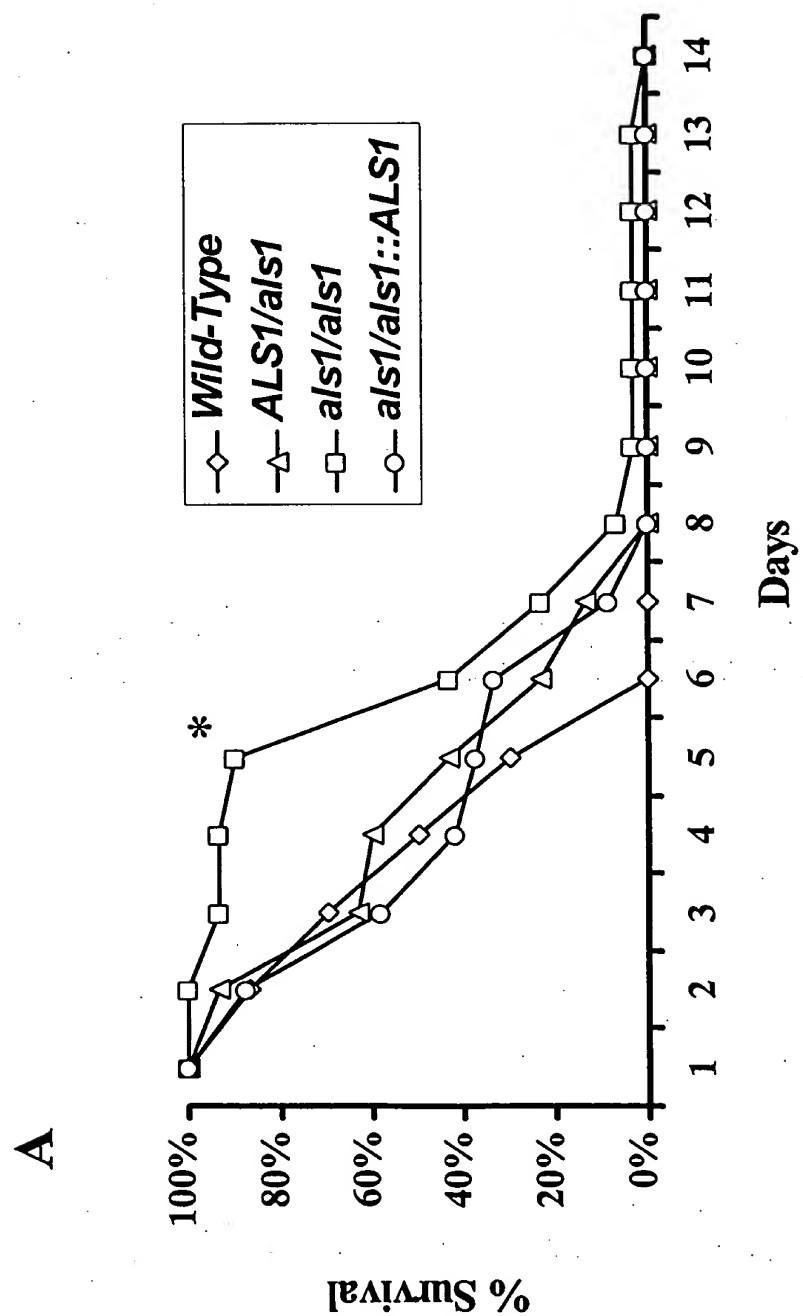


FIGURE 5A

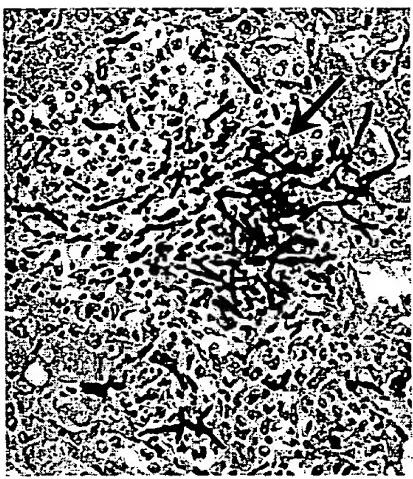


**B**

**a** Wild-Type



**als1/als1::ALS1**



**b** Wild-Type



**als1/als1::ALS1**

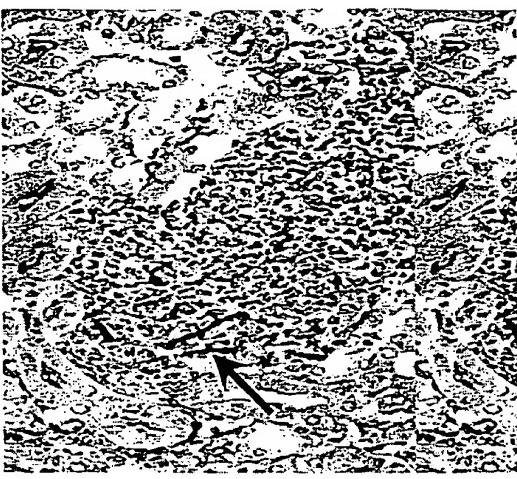
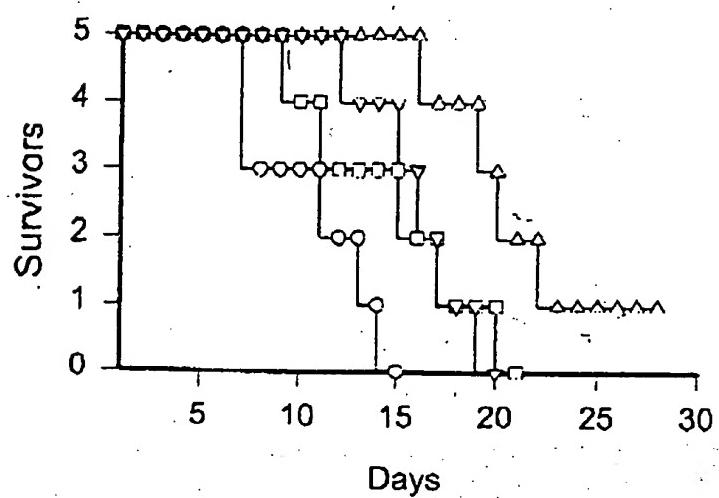


FIGURE 5B

### Prophylactic effect of antiALS antibody against disseminated candidiasis



#### MST (days)

—○— DPBS	$11.4 \pm 3.3$
—□— NRS (PB)¹	$15.4 \pm 4.4$
—△— S²-antiALS	$22.0 \pm 4.5$
—▽— I³-antiALS	$16.8 \pm 2.6$

FIGURE 6

200  
190  
180  
170  
160  
150  
140  
130  
120  
110  
100  
90  
80  
70  
60  
50  
40  
30  
20  
10

1 ATGCTTCAACAATTTACATTGTTATTCTATATTGTCATTGCAAGTGCAAAGACAATC  
1 M L Q Q F T L L F L Y L S I A S A K T I  
61 ACTGGTGTGTTGATAGTTAATTCACTGGTCCAATGCTGCTAATTATGCTTTC  
21 T G V F D S F N S L T W S N A A N Y A F  
121 AAAGGGCCAGGATACCCAACTTGAATGCTGTTGGGTTGGCCTTAGATGGTACCAAGT  
41 K G P G Y P T W N A V L G W S L D G T S  
181 GCCAATCCAGGGATACTCACATTGAATATGCCATGTGTTAAATATACTACTTCA  
61 A N P G D T F T L N M P C V F K Y T T S  
241 CAAACATCTGTTGATTAACTGCCATGGTAAATATGCTACTGTCAATTATTCT  
81 Q T S V D L T A D G V K Y A T C Q F Y S  
301 GGTGAAGAATTACAACCTTTCTACATTAACATGTACTGTGAACGACGCTTGAAATCA  
101 G E E F T T F S T L T C T V N D A L K S  
361 TCCATTAAGGCATTGGTACAGTTACCAATTGCATTCAATGTTGGTGGAACAGGT  
121 S I K A F G T V T L P I A F N V G G T G  
421 TCATCAACTGATTGGAAGATTCTAAATGTTTACTGCTGGTACCAATACAGTCACATT  
141 S S T D L E D S K C F T A G T N T V T F  
481 AATGATGGTGTAAAAGATATCTAATTGATGTTGAGTTGAAAGTCACCGTTGATCCA  
161 N D G D K D I S I D V E F E K S T V D P  
541 AGTGCATATTGTTGATGCTTCCAGAGTTATGCCAAGTCTCAATAAGGTACAACACTTTT  
181 S A Y L Y A S R V M P S L N K V T T L F  
601 GTGGCACCAATGTGAAAATGGTTACACATCTGGTACAATGGGTTCTCCAGTAGTAAC  
201 V A P Q C E N G Y T S G T M G F S S S N  
661 GGTGACGTTGCTATTGATTGCTCAAATATTCAATTGGTATCACAAAAGGATTAATGAT  
221 G D V A I D C S N I H I G I T K G L N D  
721 TGGAATTATCCGGTTCATCTGAATCATTTAGTTACACTAAAACCTTGTCACATCTAATGGA  
241 W N Y P V S S E S F S Y T K T C T S N G  
781 ATTCAAGATTAATATCAAAATGTACCTGCTGGTTATCGTCCATTATTGATGCTTATATT  
261 I Q I K Y Q N V P A G Y R P F I D A Y I  
841 TCTGCTACAGATGTTACCAATATACTTACATACCAATGATTATACTTGTGCTGGC  
281 S A T D V N Q Y T L A Y T N D Y T C A G  
901 AGTCGTCTGCAAAGTAAACCTTCACTTAACATGGACTGGATACAAGAATAGTGATGCC  
301 S R L Q S K P F T L R W T G Y K N S D A  
961 GGATCTAACGGTATTGTCATTGTTGCTACAACACTAGAACAGTTACAGACAGTACCACTGCT  
321 G S N G I V I V A T T R T V T D S T T A  
1021 GTCACTACTTACCAATTCAATCCAAGTGTGATAAAACCAAAACAATCGAAATTTGCAA

FIGURE 7

2063

341	V T T L P F N P S V D K T K T I E I L Q
1081	CCTATTCCAACCACTACCATCACAACTTCATATGTTGGTGTGACTACTTCCTATCTGACT
361	P I P T T T I T T S Y V G V T T S Y L T
1141	AAGACTGCACCAATTGGTAAACAGCTACTGTTATTGTTGATGTGCCATATCATACTACC
381	K T A P I G E T A T V I V D V P Y H T T
1201	ACAACCTGTTACCACTGAATGGACAGGAACAATCACTACCACCAACTCGTACCAATCCA
401	T T V T S E W T G T I T T T T R T N P
1261	ACTGATTCAATTGACACAGTGGTGTACAAGTCCACTGCCAAATCCAACGTGTTAGTACT
421	T D S I D T V V V Q V P L P N P T V S T
1321	ACTGAATATTGGTCTCAGTCCTTGCTACAACCACTACAGTTACTGCTCCTCCAGGTGGT
441	T E Y W S Q S F A T T T T V T A P P G G
1381	ACCGATACTGTGATTATCAGAGAGCCACCAAACCATACTGTCACTACTACTGAATATTGG
461	T D T V I I R E P P N H T V T T T E Y W
1441	TCACAATCCTTGCTACTACTACTGTTACTGCTCCTCCAGGTGGTACTGACTCAGTA
481	S Q S F A T T T V T A P P G G T D S V
1501	ATTATCAGAGAACCAACCAAATCCAACGTGCACTACAACCGAGTATTGGTCTCAATCCTTT
501	I I R E P P N P T V T T T E Y W S Q S F
1561	GCTACTACTACAGTTACTGCTCCTCCAGGTGGTACTGACTCAGTAATTATCAGAGAA
521	A T T T T V T A P P G G T D S V I I R E
1621	CCTCCAAACCCAACGTCAACCACCACTGAATATTGGTCCCAATCTACGCAACCAAC
541	P P N P T V T T E Y W S Q S Y A T T T
1681	ACTGTGACTGCTCCTCCAGGAGGCAGTGAACGTAATTATCAGAGAACCAACCAAC
561	T V T A P P G G T D S V I I R E P P N H
1741	ACTGTCACTACTGAATACTGGTCACAAATCATATGCCACCACTACCACTGTAACGTCA
581	T V T T E Y W S Q S Y A T T T T V T A
1801	CCACCAGGTGGTACTGACACTGTTATCATTAGAGAGCCACCAAACCAACTGTCAC
601	P P G G T D T V I I R E P P N H T V T T
1861	ACTGAGTATTGGTCTCAATCGTTGCTACTACCACCAACTGTAACGTGTCACCAAGTGGC
621	T E Y W S Q S F A T T T V T G P P S G
1921	ACTGATACTGTTATCATTAGGAAACCAACCAAACCAACTGTCACCACTACTGAATACTGG
641	T D T V I I R E P P N P T V T T T E Y W
1981	TCTCAATCATATGCAACCACTACTACCAATTACCGCTCCACCTGGTGAACGTGATACCGTT
661	S Q S Y A T T T I T A P P G E T D T V
2041	CTTATCAGAGAGCCACCAAACCAACTGTCACCACTACTGAATACTGGTCTCAATCATAT
681	L I R E P P N H T V T T T E Y W S Q S Y
2101	GCTACAACCAACCACTGTTACTGACCCACCTGGTGAACCGATACCGTTCTATCAGAGAG
701	A T T T T V T A P P G E T D T V L I R E
2161	CCACCAAACCAACTGTCACCACTACTGAATACTGGTCTCAATCATATGCTACAAACCAAC

FIGURE 7

721 P P N H T V T T E Y W S Q S Y A T T T  
 2221 ACTGTTACTGCACCACCAAGGGTACCGATACTGTTATCATTAGAGAGCCACCAAATCCA  
 741 T V T A P P G G T D T V I I R E P P N P  
 2281 ACAGTTACTACTGAATATTGGTCACAATCATTGCCACAACCACAGTTACTGCT  
 761 T V T T T E Y W S Q S F A T T T T V T A  
 2341 CCTCCAGGTGGTACTGACACTGTGATTATCTATGAAAGCATGTCAAGTTCAAAGATTCT  
 781 P P G G T D T V I I Y E S M S S S K I S  
 2401 ACATCCTCCAATGATATAACCAGTATCATTCCATCATTCCGTCCTCATTATGTCAAC  
 801 T S S N D I T S I I P S F S R P H Y V N  
 2461 AGCACAACCTCCGATTGTCAACATTGAAATCTTCATCCATGAATACTCCTACTTCTATC  
 821 S T T S D L S T F E S S S M N T P T S I  
 2521 AGTAGTGATGGTATGTTGTCCTCTACAACCTTGTTACTGAATCAGAAACAACATACA  
 841 S S D G M L L S S T T L V T E S E T T T  
 2581 GAACTGATTGCACTGATGGTAAAGAGTGTCTAGATTGTCCAGTTCTCTGGTATTGTC  
 861 E L I C S D G K E C S R L S S S S G I V  
 2641 ACAAACTCCAGATAGCAATGAATCCTCAATCGTAACTAGTACTGTTCCACTGCAAGTACA  
 881 T N P D S N E S S I V T S T V P T A S T  
 2701 ATGTCGATTCACTTCTTCAACTGATGGTATTAGTGTACATCTCTGATAATGTTCA  
 901 M S D S L S S T D G I S A T S S D N V S  
 2761 AAATCAGGAGTATCAGTTACAACCGAAACTCTGTTACAACATTCAAACACTCCAAAC  
 921 K S G V S V T T E T S V T T I Q T T P N  
 2821 CCATTATCATCTTCAGTGACATCATTGACTCAGTTGTCCTCAATTCCAAGTGTTCAGAA  
 941 P L S S S V T S L T Q L S S I P S V S E  
 2881 AGTGAAGTAAAGTTACATTACAAGCAATGGAGACAACCAAGTGGTACTCATGATTCA  
 961 S E S K V T F T S N G D N Q S G T H D S  
 2941 CAATCTACTTCACTGAAATTGAAATTGTAACAACCAACAGTTCTACTAAAGTTTACCACT  
 981 Q S T S T E I E I V T T S S T K V L P P  
 3001 GTCGTTCTTCTAATACTGATTTGACTAGTGAACCAACAAATACCAAGAGAACACCAACT  
 1001 V V S S N T D L T S E P T N T R E Q P T  
 3061 ACATTATCAACTACTCAAACCTCCATCACTGAAGATATCACCAACATCTCAACCTACAGGT  
 1021 T L S T T S N S I T E D I T T S Q P T G  
 3121 GATAATGGAGACAATACTTCATCAACCAATCCAGTTCAACTGTGGCAACAAGTACTTTA  
 1041 D N G D N T S S T N P V P T V A T S T L  
 3181 GCATCTGCAAGTGAAGAAGACAACAAAAGCGGTTCTCATGAATCAGCATCCACAAGTTG  
 1061 A S A S E E D N K S G S H E S A S T S L  
 3241 AACCAAGTATGGGTAAAATTCTGGATTAACACTTCACTGAAATTGAAGCTACAACA  
 1081 K P S M G E N S G L T T S T E I E A T T  
 3301 ACCAGTCCTACAGAAGCTCCATCACCTGCTGTTCTGGTACTGATGTAACACTGAA

FIGURE 7

1101 T S P T E A P S P A V S S G T D V T T E  
 3361 CCAACTGATACTAGAGAACAAACCTACTACATTATCAACTACTTCAAAAACAAACAGTGAA  
 1121 P T D T R E Q P T T L S T T S K T N S E  
 3421 CTGGTTGCTACTACACAAGCTACTAATGAAAATGGTGGTAAATCTCCATCAACTGATTAA  
 1141 L V A T T Q A T N E N G G K S P S T D L  
 3481 ACATCAAGCTTGACAACAGGCACCTCAGCATCTACAAGTGCTAATAGCGAACTTGTACT  
 1161 T S S L T T G T S A S T S A N S E L V T  
 3541 AGTGGATCTGTTACTGGTGGAGCTGTTGCCAGTGCTCAAATGATCAATCACATTCTACT  
 1181 S G S V T G G A V A S A S N D Q S H S T  
 3601 TCTGTTACCAACAGCAACAGCATTGTATCTAATACCCCACAAACTACATTGAGTCACAA  
 1201 S V T N S N S I V S N T P Q T T L S Q Q  
 3661 GTTACCTCATCCTCACCTCAACCAACACATTCTACATACGATGGCTCTGGT  
 1221 V T S S S P S T N T F I A S T Y D G S G  
 3721 TCTATTATCCAACATTCTACTTGGTTGACGGTTGATCACATTATTGTCCTTGTTCATT  
 1241 S I I Q H S T W L Y G L I T L L S L F I  
 3781 TAGTGA  
 1261 \* \*

FIGURE 7